



iTRAQ ratio of BSA

116 / 114	1.005
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Sequence	# PSMs	# Proteins	# Protein Groups	# Missed Cleavages	116/114	116/114 Count
MPCTEDYLSLILNR	4	1	1	0	1.54	2
DAFLGSFLYEYSR	4	1	1	0	1.15	2
KQTALVELLK	4	1	1	1	0.85	2
GLVLIAFSQYLQQCPFDEHVK	4	1	1	0	2.10	2
KVPQVSTPTLVEVSR	4	4	2	1		
SLHTLFGDELCK	4	1	1	0	1.06	2
RHPEYAVSVLLR	2	1	1	1	0.87	1
RPCFSALTPDETYVPK	2	1	1	0	1.06	1
LFTFHADICTLPDTEK	3	1	1	0	0.87	1
FKDLGEEHFK	4	1	1	1	0.99	2
AEFVEVTK	2	1	1	0	1.02	2
LGEYGFQNALMR	3	1	1	0		
LVNELTEFAK	4	1	1	0	1.05	2
HLVDEPQNLIK	4	1	1	0	1.06	2
CCTKPESERMPCTEDYLSLILNR	2	1	1	1	0.80	1
QTALVELLK	3	1	1	0	0.91	1
LCVLHEK	2	1	1	0	0.80	1
CCTESLVNR	2	4	2	0		
YLYEIAR	1	4	2	0		
LVTDLTK	2	4	2	0		
LSQKFPK	1	1	1	1	0.81	1